

FIG. 1.

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2/12

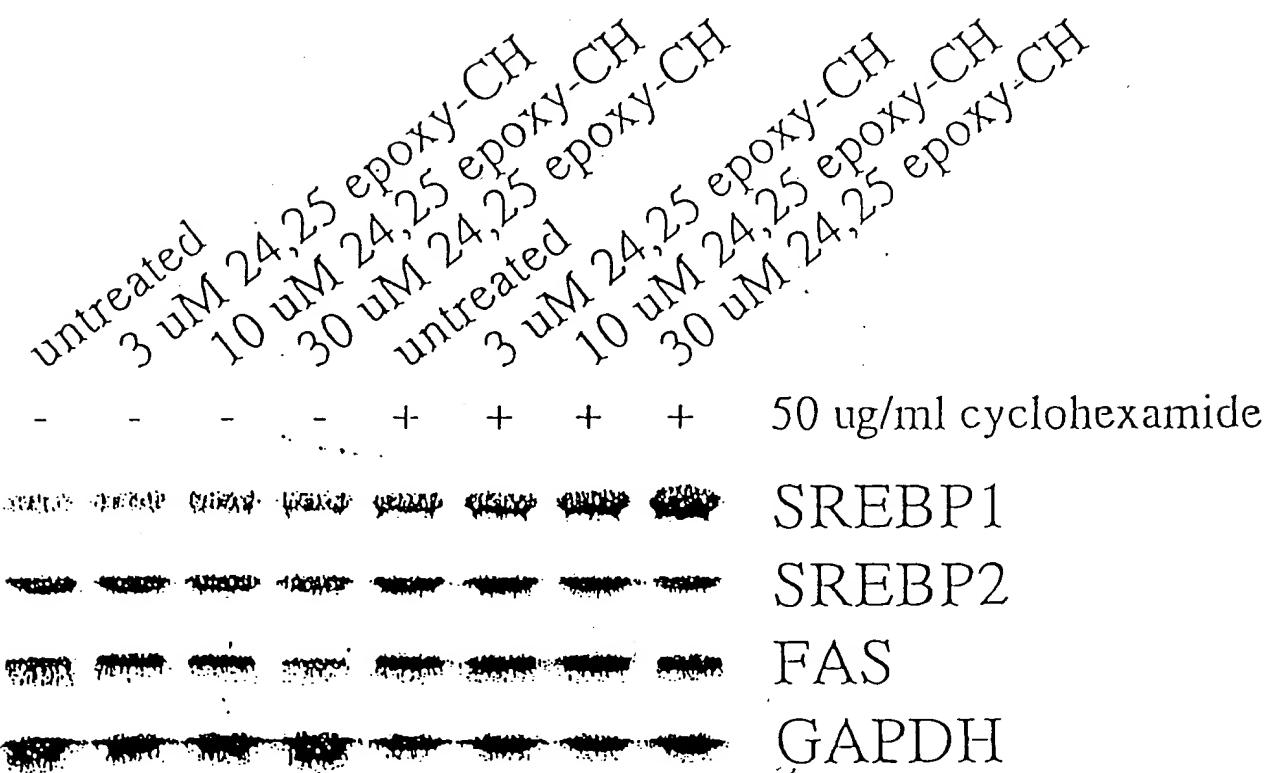


FIG. 2.

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Appln. No.: 09/848,990
Filed: May 3, 2001
**TREATMENT OF HYPERTRIGLYCERIDEMIA AND OTHER
CONDITIONS USING LXR MODULATORS**
Replacement Sheet

3/12

35

CaCO_3

293

HepG2

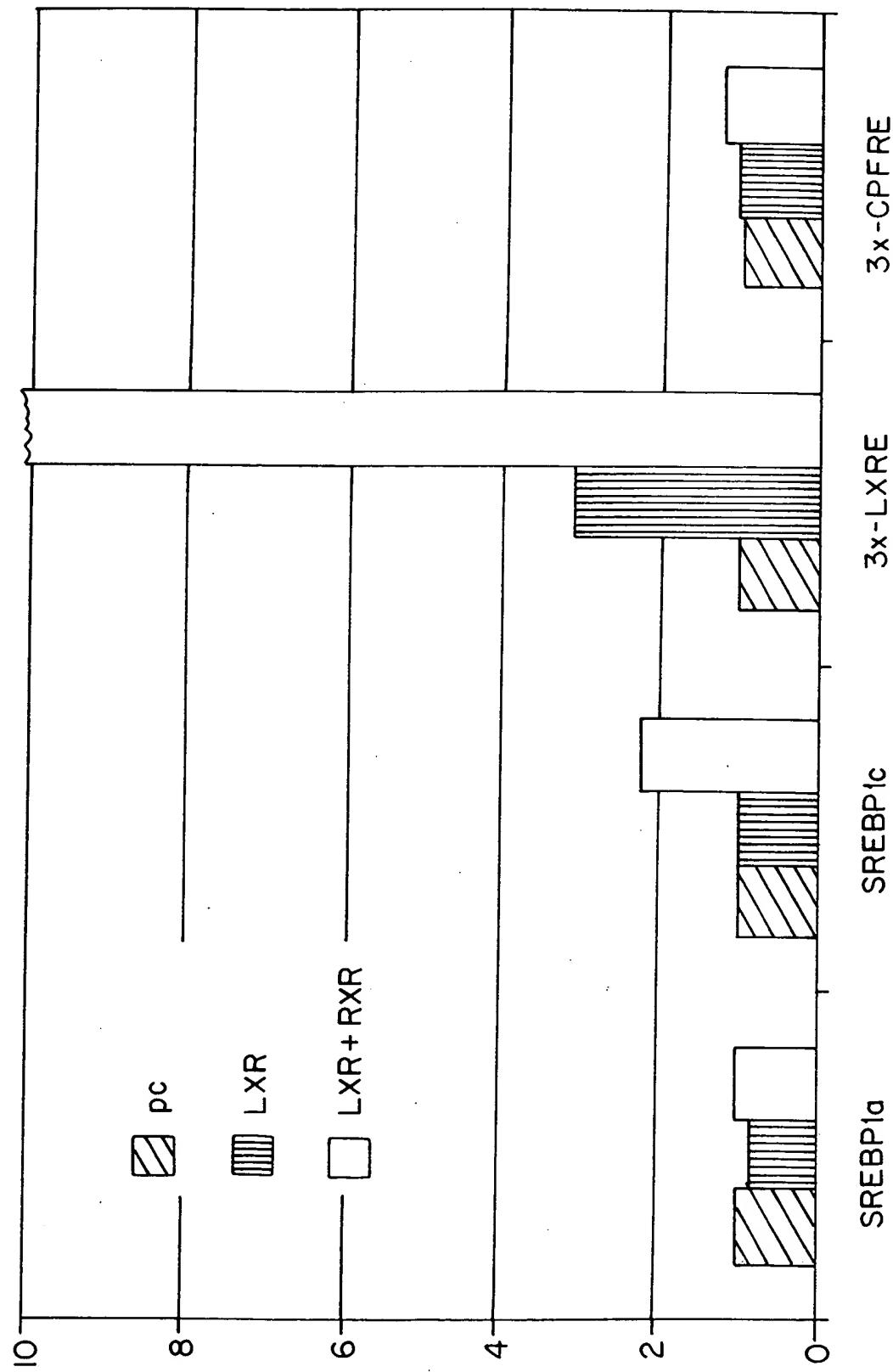
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CONDITIONS USING LXR MODULATORS
Replacement Sheet

4/12



FOLD OF ACTIVATION

FIG. 4.

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Appn. No.: 09/848,990

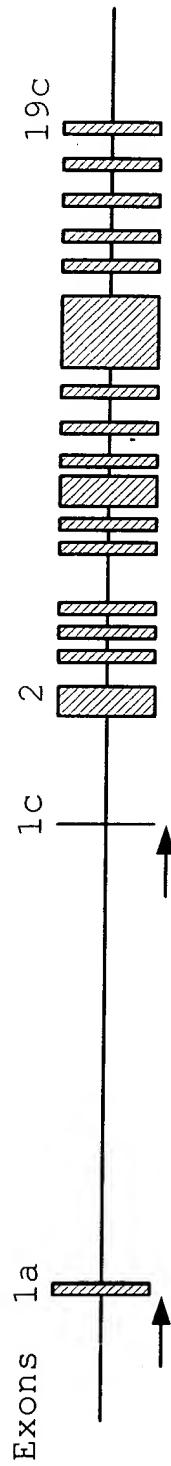
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TREATMENT OF HYPERTRIGLYCERIDEMIA AND OTHER
CONDITIONS USING LXR MODULATORS

Replacement Sheet

5/12

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in SREBP1c promoter

TTGGGACCTGGCATATGGAAAGGGCTTGGGGTGCAGGTGTGTCCCTGGCCCCAGCACTGCCACACCCCTCGGT

TGACCTCACTTTGCCCTCTGAGCCAGAACCTCTGAGGGCAGCTCAGGGATAACCTTTCCCTCGATGCCCTT

GGGAACATGCCCTCGCCCTGCTATCTGAGCCCTGGCTTCCCCAAAGCCATCATAGACCCCTACCTCCTAT

ATGGAGGCCATGGAATGCTTGGGTACATGCCGCCACCCCTGCCCTCCCTCTGGTAGGGCTAGGTGG

TGGCAGAGCCCCACCTGGCAGGGTTACATGCCGCCACCCCTGCTTGGTAGGGCTAGGTGG

AGGCCTCACTCTCTGCATCTTAGTTCTTCACTAAATGCTATTCAATGCCCTGCCTGAGGGTGGTGGG

CGTGAGTAAGTGGAGAGAACGCCCTCAGCCAGGGACCCCATATGCTTAACATCCAGACACCAAGGGCCACTCA

CAGCAGCCGGCTTGTGTTCGTCATCCCTTGGTAGGGAACTGGGACGCTGGACTCCAGATCTCCAGGAGGCC

CAGACTAGGGCGGAAGGAGGGCTCAGCCCTGAGCTGAATAACCTAGAATAACCCAGCCCCACTCCC

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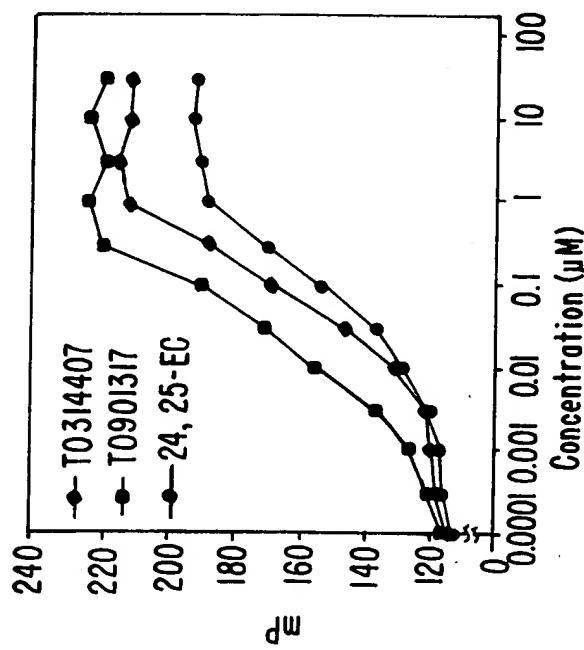
CGAAGgtattttggggccctccacac

FIG. 5.

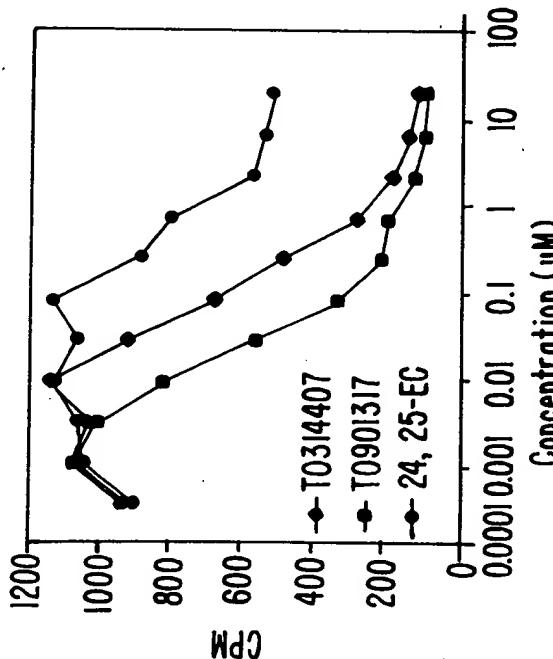
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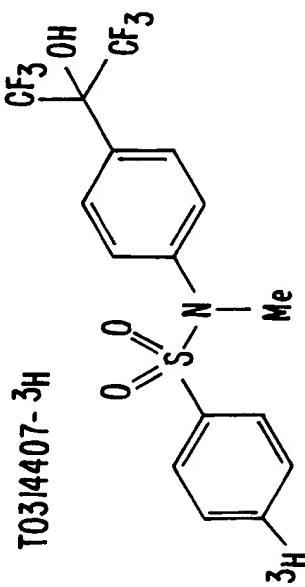
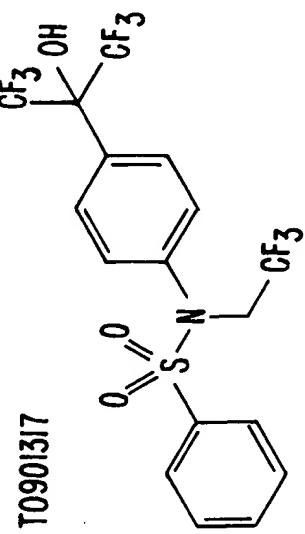
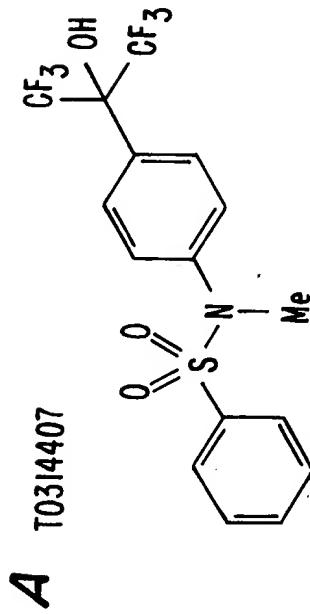
6/12



B



C



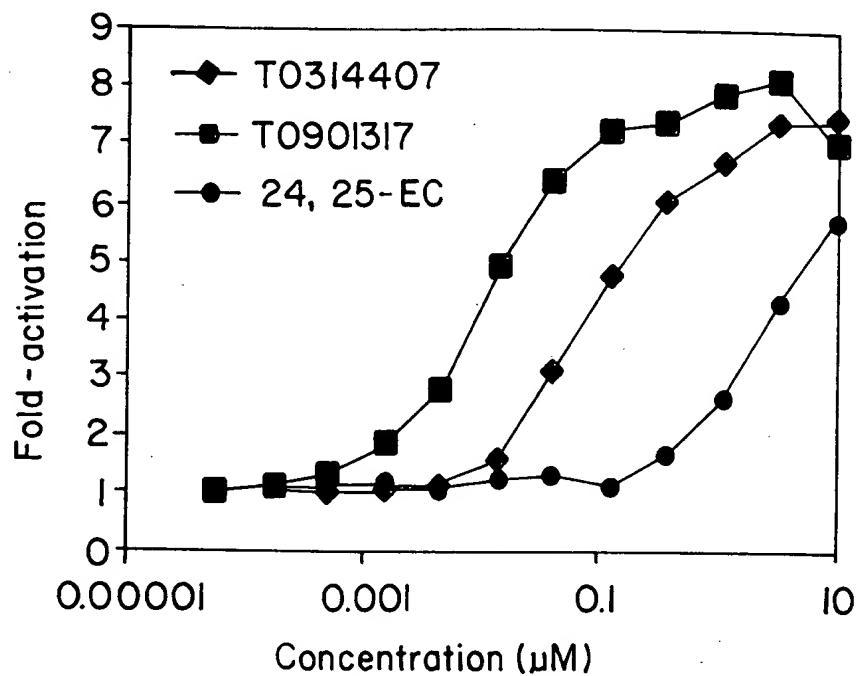
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FIG. 6.



7/12

A



B

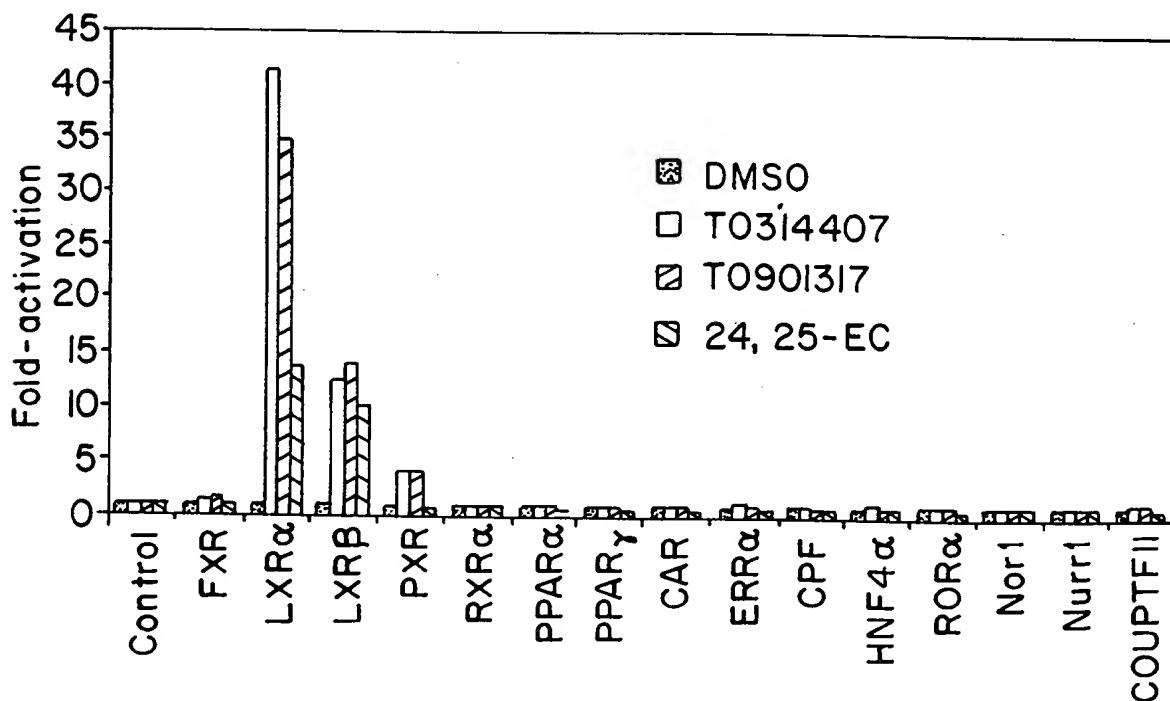


FIG. 7.

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TREATMENT OF HYPERTRIGLYCERIDEMIA AND OTHER

CONDITIONS USING LXR MODULATORS

Replacement Sheet

8/12

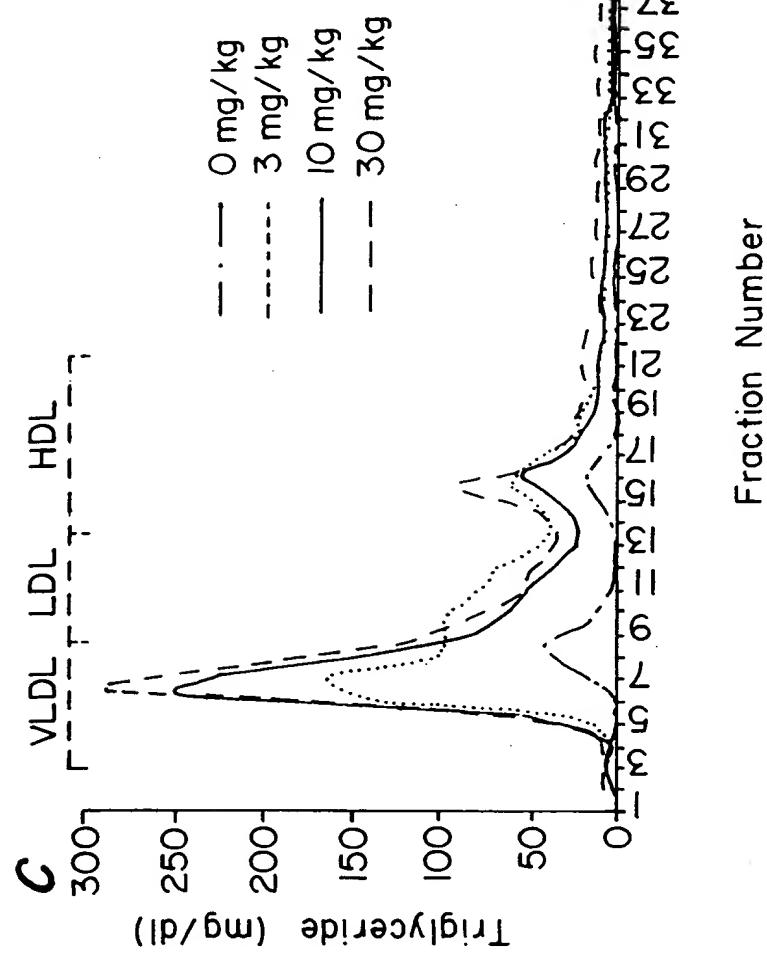
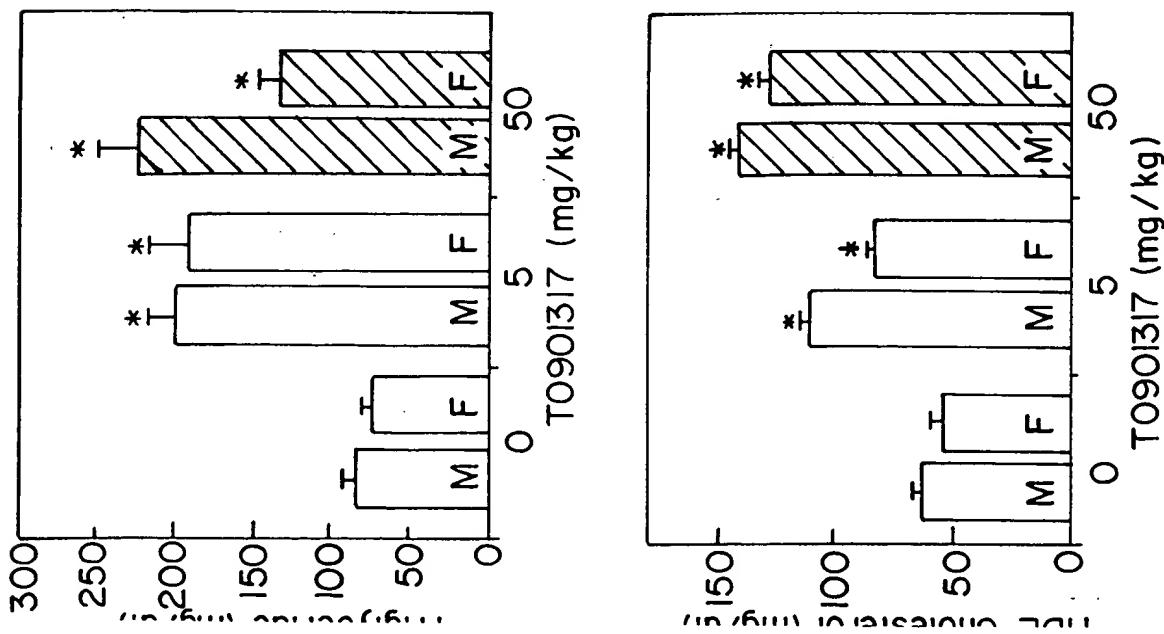


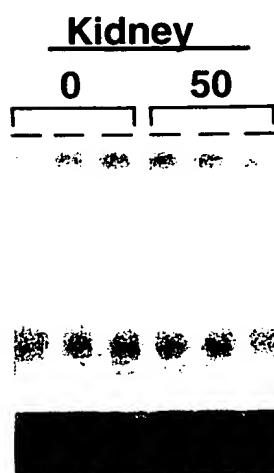
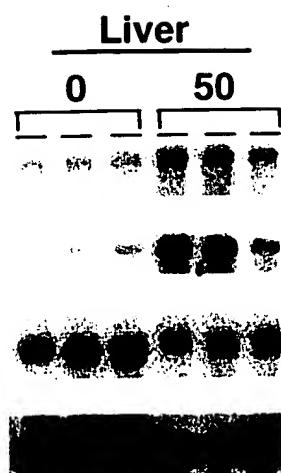
FIG. 8.

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9/12



mg/kg T0901317

Acetyl CoA Carboxylase

Fatty Acid Synthase

Squalene Synthase

HMG CoA Synthase



B T0901317 (mg/kg)

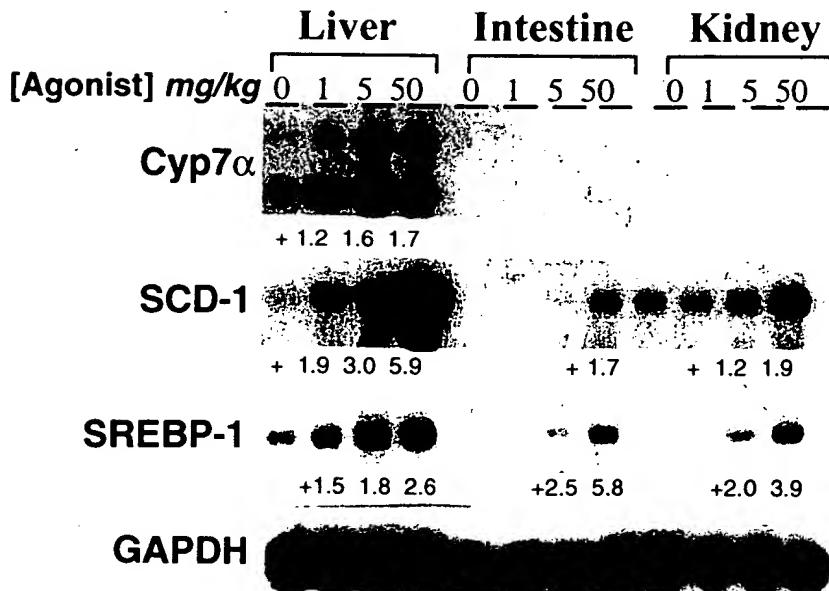
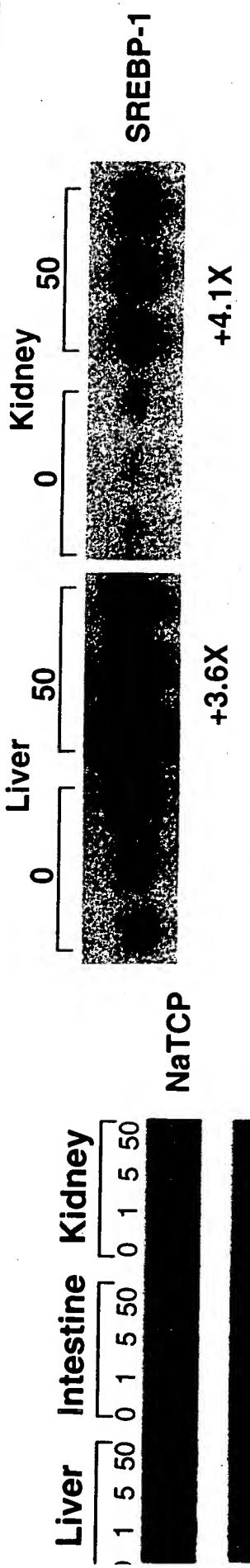


FIG. 9

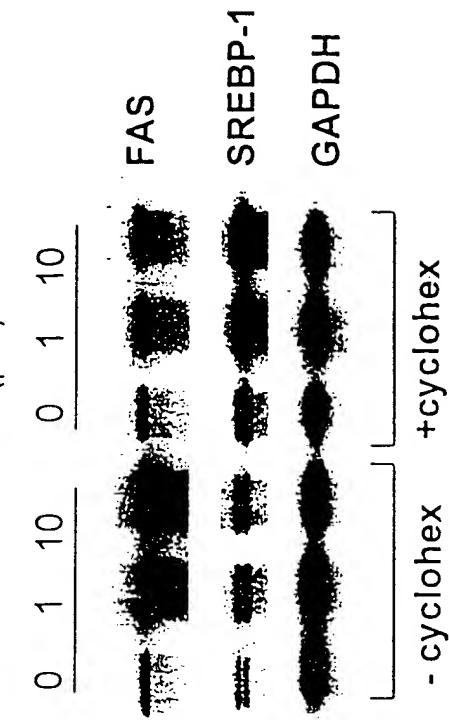
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D T0901317 [mg/kg]



E T0314407 (μ M)



F/G. 9. (Continued)

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11/12

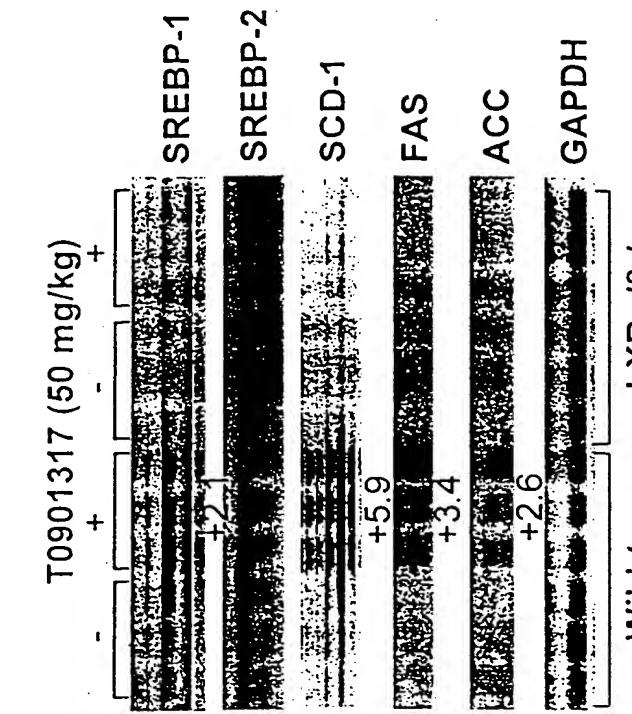
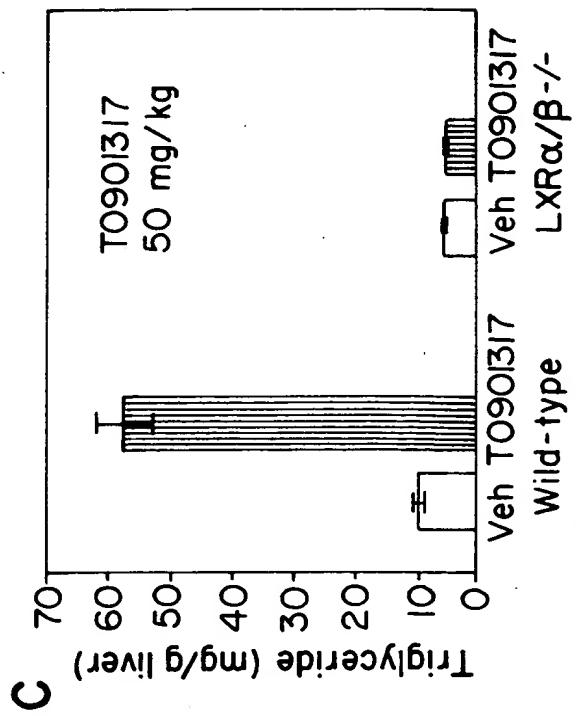
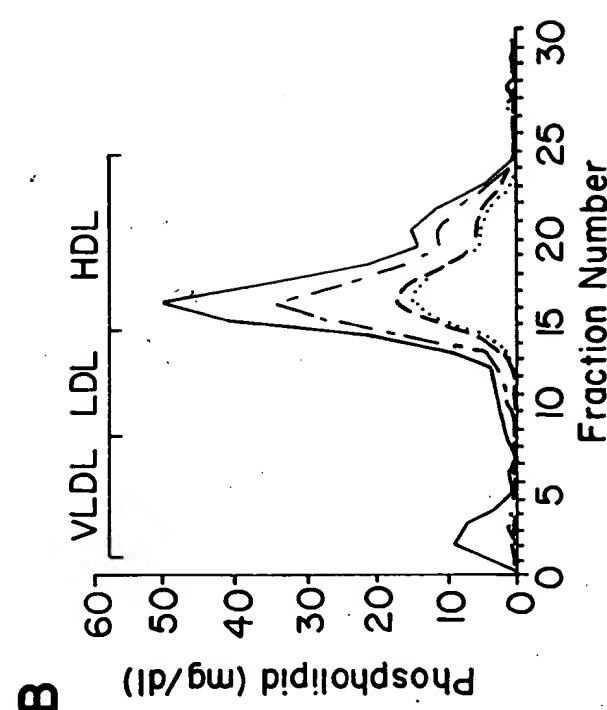
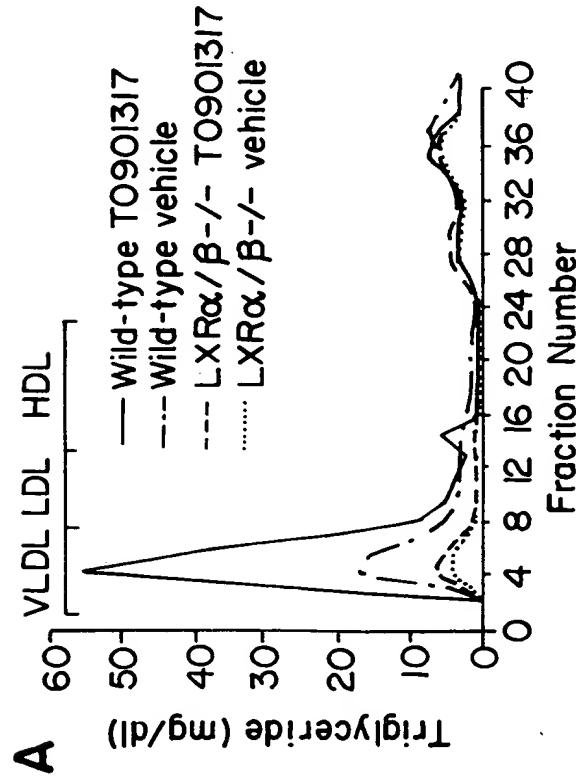


FIG. 10.

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12/12

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DN _A Probe	Primer Set	Primer Sequence	PCR Product Length
ethyl CoA carboxylase	5' 3'	TACCTGTGGACAGCAACCA TGGTCGACAGCAAGGGAA	521
ty acid synthase	5' 3'	CCCGATGGGGTTTCATC GATCCCTCTGGTGTCCC	493
valene synthase	5' 3'	CGTCAGTGCTGAATGAACT TTGGGATCCGGTGATAAAT	288
lG CoA synthase	5' 3'	CCCAGCAGGGTTTCTACAA AATTCCCTCAGGGGACATGC	1285
lEBP-1	5' 3'	TCA ACAACCAAGGACAGTGACTTCCCTGGCC GTTCTCCCTGCTTGAGCTTCTGGTTGCTGTG	1028
CP	5' 3'	AGCAAGATCAAGGCTCACTTCT ATAGTGTGGCCCTTTGGACTC	405
TP	5' 3'	TTCTCTGCTTCTCTCCCTCCTA GGCTCGTTTCA TAGGAGTAGA	403
lOA-I	5' 3'	GGCAGAGACTATGTGTCCCAGTTGA GTCATCCAGCGGGTTGGCTTCTC	564
lOA-II	5' 3'	ATAGTCTGCCATCATGAAGCTG GAGAAAACAGGCAGAAGGTAGG	406
lOE	5' 3'	CCGTGCTGTTGGTCACATT TTATAAGCAAGGGCCACCA	1014

FIG. 11.